Sequencing, Finishing, and Analysis in the Future (SFAF)
La Fonda on the Plaza, Santa Fe, NM: June 1st - 3rd, 2016

Call for Abstracts (both talks and posters) Deadline March 28th, 2016

Please join us for the **11th annual** "Sequencing, Finishing and Analysis in the Future" Meeting on Wednesday, **June 1st through June 3rd** in beautiful, historic Santa Fe, NM. The three-day SFAF conference will focus on Next Generation Sequencing technologies, applications, and their effect on the rapidly advancing field of Genomics.

Keynote Speakers:
- **Pavel Pevzner, Ph.D.,** Ronald R. Taylor Professor of Computer Science and Director of the NIH Center for Computational Mass Spectrometry at University of California, San Diego.
- TBA
- TBA

Areas to be emphasized include, but are not limited to the following:

Genome Sequencing:
- Sequencing strategies and technology advancements using the various NGS platforms
- *De novo* sequencing, re-sequencing, Human seq., RNA seq., metagenomics, etc.
- Sequencing applications for Metagenomics, Transcriptomics, Diagnostics, and Biosurveillance

Genome Assembly:
- Whole genome assemblers and integration of next generation data
- *De novo* assemblers for short reads, hybrid assemblers
- Single cell and metagenomic assemblies

Genome Improvement:
- Next Generation Finishing tools, technologies, and pipelines
- Human Genomics and genome improvement
- Quality standards for new technologies and mixed data sets
- Single cell / cell sorting and metagenomic finishing

Genome Analysis:
- Genome annotation and pathway identification tools and pipelines
- Comparative genomics, re-sequencing, SNPs, structural variation
- Large scale data management, cloud computing
- Analysis for Metagenomics, Antimicrobial Resistance, and Forensics

Applications of NGS:
- Bringing sequence to the clinic (i.e. diagnostics)
- Human, non-human, and infectious disease applications
- Gene Editing, Synthetic Genomics, Forensics, and Biosurveillance

The conference is being sponsored by numerous genomics/sequencing vendors and hosted by the Los Alamos National Laboratory, thus **NO** registration fee is required. Participants need to cover travel costs, hotel and dinner charges. Breakfast, lunch and snacks will be provided. A block of rooms (**SFAF**) are reserved at the La Fonda at a special conference rate of $99 /night. **A limited number of extra rooms are also available the weekend before & after the conference for those that want to enjoy the area a little longer (Reserve using hotel link ASAP).**

Registration is limited to 220; please register soon if you plan to attend. **To register, submit an abstract, or obtain more information as it becomes available please visit our web site, http://www.lanl.gov/finishinginthefuture/ Hotel Reservations or our SFAF Registration and Abstract Submission links.** Additionally, we plan to have a job board up at the meeting this year, so please make use of this if you would like to post a job vacancy or if you are looking for something new to try out!

If you have any questions, or would like further information, please contact Chris Detter at (505) 699-1996 or SFAFmeeting@gmail.com or Shannon Johnson at shannonj@lanl.gov

We look forward to seeing you there!!!

The 2016 "Sequencing, Finishing and Analysis in the Future" Organizing Committee:
- * Chris Detter, Ph.D., Chief Science Advisor, MRIGlobal
- * Johar Ali, Ph.D., Director Research, AA Ontario, Canada
- * Patrick Chain, Bioinformatics Team Leader, LANL
- * Michael FitzGerald, Microbial Special Projects Manager, Broad Institute
- * Bob Fulton, M.S., Director of Project Development & Management, WashU
- * Darren Grafham, Lab Manager, Children's Hospital, Sheffield, UK
- * Alla Lapidus, Ph.D., Director, Center for Algorithmic Biotechnology SPbSU, Russia
- * Donna Muzny, M.Sc., Director of Operations, BCM
- * Shannon Dugan-Perez, Project Manager, BCM
- * David Bruce, Project and Program Manager of Genomic Sciences, LANL
- * Shannon Johnson, Ph.D., Project Manager, LANL

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